

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 27, 2001, 16:54:43 ; Search time 28.15 seconds
(without alignments)
633.209 Million cell updates/sec

Title: US-09-830-647-2

Perfect score: 1206

Sequence: 1 MNSGAMRHSKHGFGQGIQV.....LKKPPVKVEDMSQSPAVHLM 234

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: PIR68:*
2: pir1:*
3: pir2:*
4: pir3:*
5: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	784	65.0	601	2 T02633	hypothetical prote
2	101.5	8.4	779	2 T01304	hypothetical prote
3	100.5	8.3	615	2 S38088	hypothetical prote
4	94	7.8	1415	2 S52267	DNA polymerase III
5	91	7.5	908	2 S51293	probable membrane
6	91	7.5	994	1 A47474	NAD+ ADP-ribosyltr
7	90	7.5	219	2 C71827	cag island protein
8	89	7.4	710	2 S26006	hypothetical prote
9	89	7.4	871	2 T48502	hypothetical prote
10	89	7.4	1119	2 B70126	surface-localized me
11	87.5	7.3	392	2 B70342	conserved hypochet
12	87.5	7.3	506	2 T28810	hypothetical prote
13	87.5	7.3	520	2 A71564	hypothetical prote
14	87.5	7.3	885	2 B69783	transposon homolo
15	87	7.2	426	2 F82315	conserved hypochet
16	86.5	7.2	690	2 T34149	hypothetical prote
17	86.5	7.2	1274	2 T02635	DI protein homolog
18	86.5	7.2	1462	2 T06819	DNA topoisomerase
19	86	7.1	1081	2 T15692	hypothetical prote
20	85	7.0	273	2 E81330	probable periplasm
21	85	7.0	602	2 D69331	probable DNA topoi
22	85	7.0	773	2 T00502	probable receptor-
23	84.5	7.0	299	2 S34588	senescence marker
24	84.5	7.0	942	2 JC7316	testicular zinc fi
25	84.5	7.0	1891	2 T13594	hypothetical prote
26	84.5	7.0	1920	2 T13893	gene hindsight pro
27	84	7.0	324	2 G81330	probable phosphata
28	84	7.0	1059	1 A35210	ferroxidase (EC 1.
29	83.5	6.9	362	2 T48564	probable serine rl

30	83.5	6.9	833	2 H72205	mallose ABC transp
31	83.5	6.9	1079	2 T18356	membrane protein p
32	83.5	6.9	5105	2 T32650	hypothetical prote
33	83	6.9	650	2 A35551	dnak-type molecula
34	83	6.9	1176	2 S66771	hypothetical prote
35	83	6.9	1319	2 T28203	probable DNA-dirc
36	83	6.9	1854	2 T13576	hypothetical prote
37	82.5	6.8	244	2 T25531	hypothetical prote
38	82.5	6.8	430	2 T25623	hypothetical prote
39	82.5	6.8	434	2 G64444	amidase - Methanoc
40	82.5	6.8	482	2 A30198	dihydroliipamide S
41	82.5	6.8	592	2 LLBY	actin-binding prot
42	82.5	6.8	946	2 A71843	d-lactate dehydrog
43	82.5	6.8	1225	2 A49464	chromosome segrega
44	82	6.8	287	1 MNVNRV	nonstructural prot
45	82	6.8	304	2 JX0209	lectin, galactose/

ALIGNMENTS

RESULT 1
T02633
hypothetical protein RG135C18.1 - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 05-Nov-1999
C/Accession: T02633
R:Kellen, J.; Burkhardt, J.
submitted to the EMBL Data Library, June 1998
A:Description: The sequence of Homo sapiens BAC clone RG135C18.
A:Reference number: 214683
A:Accession: T02633
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-601 <KEL>
A:Cross-references: EMBL:AC005164; NID:93242749; PIDN:AC23786.1; PID:93242750
C:Genetics:
A:Map position: 7
A:Insertions: 60/3; 77/3; 101/1; 126/3; 139/1; 154/2; 197/2; 235/3; 277/2
A>Note: WDCSC:RG135C18.1

Query Match 65.0%; Score 784; DB 2; Length 601;
Best Local Similarity 100.0%; Pred. No. 3.1e-55;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 RVEEFLSKDISYLSNKKKFAQTIGRISPPSPESAATTAETTSPPHSHDSSFKSPDT 133
|||||
Db 1 RVEEFLSKDISYLSNKKKFAQTIGRISPPSPESAATTAETTSPPHSHDSSFKSPDT 60

QY 134 VCLSRGKLVEKAIKDHDFIPSNISLSNALSWGVIKLIHIDIRYIEOKKELYLLKSS 193
|||||
Db 61 VCLSRGKLVEKAIKDHDFIPSNISLSNALSWGVIKLIHIDIRYIEOKKELYLLKSS 120

QY 194 TSVRDGGRVSGAOKTRTGRLKKPFVKVEDMSQ 227
|||||
Db 121 TSVRDGGRVSGAOKTRTGRLKKPFVKVEDMSQ 154

RESULT 2
T01304
hypothetical protein T14P8.6 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 18-Feb-2000
C/Accession: T01304
R:Kalicki, J.; Elliott, G.; Cloud, J.
submitted to the EMBL Data Library, May 1998
A:Description: The sequence of A. thaliana T14P8.
A:Reference number: Z14290
A:Accession: T01304
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-779 <KAL>

A:Molecule type: DNA
 A:Residues: 1-908 <MAN>
 A:Cross-references: EMBL:Z71597; NID:g1302433; PID:e239767; PID:g1302434; MIPS:YNL321w
 A:Experimental source: strain S288C
 C:Genetics:
 A:Map position: 14L
 C:Keywords: transmembrane protein
 C:Keywords: transmembrane #status predicted <TM1>
 F:250-266/Domain: transmembrane #status predicted <TM2>
 F:413-422/Domain: transmembrane #status predicted <TM3>
 F:496-512/Domain: transmembrane #status predicted <TM4>
 F:531-547/Domain: transmembrane #status predicted <TM5>
 F:561-577/Domain: transmembrane #status predicted <TM6>
 F:595-611/Domain: transmembrane #status predicted <TM7>
 F:631-647/Domain: transmembrane #status predicted <TM8>
 F:689-705/Domain: transmembrane #status predicted <TM9>
 F:748-764/Domain: transmembrane #status predicted <TM10>
 F:820-836/Domain: transmembrane #status predicted <TM11>
 F:886-902/Domain: transmembrane #status predicted <TM12>

Query Match 7.5%; Score 91; DB 2; Length 908;
 Best Local Similarity 31.1%; Pred. No. 23;
 Matches 41; Conservative 19; Mismatches 42; Indels 30; Gaps 9;

OY 32 LKIDRPEKSKCKP-----LW--GKVFYLDLPSVTISEKIDKIDLGKVEEFLSKDI 83
 DB 271 LVTSNAKEYSKCLYKILANTFLMPFGKMYL-----IODEQYIODED KDEGISMOQFYMWYT 325

OY 84 SY--LISNKKKAKPAQTIGRISPVSPESAY--TAETI-----SPHSHDGSSEKSPD 132
 DB 326 SYSNRLVFHQSQAQKFOOR--EDHPAPATRTSSSLMPAPTATTAPLNSNHSYNSIRHEITH 383

OY 133 TWC-----LSRGR 140
 DB 384 AAAGRRYFGRGR 395

RESULT 6
 A:M7474
 NAD+ ADP-ribosyltransferase (EC 2.4.2.30) - fruit fly (Drosophila melanogaster)
 C:Species: Drosophila melanogaster
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
 C:Accession: A47474
 R:Uchida, K.; Hanei, S.; Ishikawa, K.; Ozawa, Y.; Uchida, M.; Sugimura, T.; Miwa, M.
 Proc. Natl. Acad. Sci. U.S.A. 90, 3481-3485, 1993
 A:Title: Cloning of cDNA encoding Drosophila poly(ADP-ribose) polymerase: leucine zipper
 A:Reference number: A47474; MUID:93334521
 A:Accession: A47474
 A:Status: preliminary
 A:Stature: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-994 <UCH>
 A:Cross-references: GB:D13806; GB:D13807; GB:D13808; NID:g303545; PIDN:BA02964.1; PID:9
 C:Superfamily: NAD+ ADP-ribosyltransferase
 C:Keywords: DNA binding; glycosyltransferase; NAD; nucleus; pentosyltransferase

A:Gene: flybase:Parp
 A:Cross-references: Flybase:FBgn0010247
 C:Superfamily: NAD+ ADP-ribosyltransferase
 C:Keywords: DNA binding; glycosyltransferase; NAD; nucleus; pentosyltransferase

Query Match 7.5%; Score 91; DB 1; Length 994;
 Best Local Similarity 21.2%; Pred. No. 26;
 Matches 62; Conservative 46; Mismatches 80; Indels 104; Gaps 14;

OY 21 KNEKNRPSLSKTDN--RPEKSKCKPLMGKVFYLDLPSVTIS--EKLQDKIDLGR 74
 DB 356 KTFERSLSLTKKNDVLYVPTIPRISP---PLYNLKFSITIGLKNQKHELRKRIENLGRK 412

OY 75 VEEPLSKDISYLSNKKK-----AKPAQTIG-RISPV----- 105
 DB 413 FEVKISENTAIIISFELIQKKSTRMKFAEELGIIHIVPIEFIDFVADREGAIIKYNISRC 472

OY 106 -----PSPSATTAETTSHPSHD-----GSSFKSPDYICLSGKLIVKAIKDHP 152

DB 473 ICSWGTDPKSRIPKERTKSLNSISYTKSMPYSRTKVKVADGLAVDDSGLEDIA---HY 529
 OY 153 IPSNLSLNSALSGVKILHIDIR-----Y-----IEOKKRELYLLKKSSTSVYDGKRV 203
 DB 530 YDSNNKYS-----VLLGLTDIQRNKNSTYKQVLKADKKEKYYWIFRSWGR---GTNI 579

OY 204 GSG-----AOKT-----RTGRKRFVVED 224
 DB 580 GNSKLEEFDTSSAKRNFKEIYADKTGNEYEQRDNFVKRPTGRMYLEIQYD 631

RESULT 7
 cag island protein - Helicobacter pylori (strain J99)
 C:Species: Helicobacter pylori
 A:Variety: strain J99
 C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 08-Oct-1999
 C:Accession: C71927
 R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Dolg, P.C.; Smith, D.; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.
 Nature 397, 176-180, 1999
 A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric P
 A:Reference number: A71800; MUID:99120557
 A:Accession: C71927
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-219 <ARN>
 A:Cross-references: GB:AE001481; GB:AE001439; NID:g4155005; PIDN:AA06053.1; PID:g415
 A:Experimental source: strain J99
 C:Genetics:
 A:Gene: orf7

Query Match 7.5%; Score 90; DB 2; Length 219;
 Best Local Similarity 24.0%; Pred. No. 44;
 Matches 46; Conservative 31; Mismatches 71; Indels 44; Gaps 8;

OY 10 SKGHFOGIGIQVKNKRPISLSKTDNPEKSK-----CKPLMGKVFYLDLPSVT 59
 DB 53 NKDDCKGVIREINGSMK--MVCILHCEPTIMEKVESGRCGAYACKNCNRFYFIDLAKON 110

OY 60 ISER-LQKIDKIDLGKVEEFLSKDISYLI-----SKKKAEPQITIGRISPVSPESAYT 113
 DB 111 ERKKDKERKELKINKIEQKIKHLERFLIAGYKANIKESF-----IGCKNYPKCEWT 165

OY 114 AETTSHPHSDGSFSPPTVCLSRGKLIVERKAIKHDPIPSNLSLNSALSGVKILHID 173
 DB 166 A-----SMDSDCLKPCPCNRLMKR-----KFKRNEFFTATSLNMAIEPCL----- 208

OY 174 DIRVYTEORRKE 185
 DB 209 ----YINLKKE 216

RESULT 8
 S26006
 hypothetical protein - liverwort (Marchantia polymorpha) mitochondrion
 C:Species: mitochondrion Marchantia polymorpha
 C:Date: 07-May-1993 #sequence_revision 07-May-1993 #text_change 21-Jul-2000
 C:Accession: S26006
 R:Oda, K.; Yamato, K.; Ohta, E.; Nakamura, Y.; Takemura, M.; Nozato, N.; Akashi, K.; J. Mol. Biol. 223, 1-7, 1992
 A:Title: Gene organization deduced from the complete sequence of liverwort Marchantia
 A:Reference number: S25941; MUID:921114051
 A:Accession: S26006
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-710 <ODA>
 A:Cross-references: EMBL:M68929; NID:g786182; PIDN:AA09460.1; PID:g786246
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1992
 C:Genetics:
 A:Genome: mitochondrion

C:Keywords: mtochondrion

Query Match 7.4% Score 89; DB 2; Length 710;
 Best Local Similarity 26.5%; Pred. No. 24;
 Matches 54; Conservative 29; Mismatches 63; Indels 36; Gaps 10;

OY 14 FOGGQVKNENRSLKSKTDRPREKSKCKPMKGYLYDLSYITSEKLDKIDLG 73
 Db 226 FFGSI-AKSAKATTKTKANKGSRP---VTPPALGRVFDIYINI---DNLRAGYKRLKG 278
 OY 74 RVEEFLSKDISYLSNKKKFAOTLGRISPPSPESAYTAETTSPPSHDGS-----F 128
 Db 279 NVAGIDGRTRKADMTOKALELSEKELRQAVAPRP--AKRITITKP---DGSRLPLSLA 332
 OY 129 KSPDYCLSGKLYLVEKAKR-----DHDPIPSNSILS-----NLSMGVYKILMID 173
 Db 333 STVKKVQSTLKELEPHFESLFRDSSHGFRGRSCHKALRLDRYSWTALTLVQI----- 388
 OY 174 DIRYYIPQKKKEYLKSKSTSVR 197
 Db 389 DIKKDFDKIHDDL-LIKEMESVLR 411

RESULT 9
 T48502
 Hypothetical protein F15N18.20 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
 C:Accession: T48502
 R:Bayan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Bancroft, submitted to the Protein Sequence Database, April 2000
 A:Reference number: 224490
 A:Accession: T48502
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-871 <BEV>
 A:Cross-references: EMBL:AL163815
 A:Experimental source: cultivar Columbia; BAC clone F15N18
 C:Genetics:
 A:Map position: 5
 A:Introns: 562/2; 602/3; 622/3
 A>Note: F15N18.20

Query Match 7.4% Score 89; DB 2; Length 871;
 Best Local Similarity 20.2%; Pred. No. 31;
 Matches 37; Conservative 43; Mismatches 65; Indels 38; Gaps 8;

OY 30 KSLKTNRPKSKCKPLMGKXYFLDLP--SVTISEKLQDKIDLGKVEEFLSKDISYLI 87
 Db 70 KAVQTSAPQK-PAPPVNKKQHPPOKRSVKAMEEVNSVR--SKMRRESIASALALVK 125
 OY 88 SNKKEAFKQATLGRISFPVSPESAYTAETTSPPH---PSHDGSSFKSPDYCLSGRCK-- 140
 Db 126 KDDSPKSGKENGIVETVITQENTQSFQSPASISVPGVGTSEMPTESSVOKDS 185
 OY 141 -----LLVEKAKR-----DHDFTPSNSIL-----SNLSMGVYKILMID 175
 Db 186 ELPVDMVMDVLEKENVLKSQYDEVFPRDNPFDIIFPNDLLHGNELSMLEVSIDGET 245
 OY 176 RYV 178
 Db 246 KDY 248

RESULT 10
 B70126
 Surface-located membrane protein 1 (Imp1) homolog - Lyme disease spirochete
 C:Species: Borrelia burgdorferi (Lyme disease spirochete)
 C>Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 11-Jan-2000
 C:Accession: B70126
 R:Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White

son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vu
 ; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
 Nature 390, 580-586, 1997
 A:Authors: Smith, H.O.; Venter, J.C.
 A>Title: Genomic sequence of a Lyme disease spirochete, Borrelia burgdorferi.
 A:Reference number: A70100; MUID:98065943
 A:Accession: B70126
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-1119 <KLE>
 A:Cross-references: GB:AE001131; GB:AE00783; NID:92688098; PID:AMC66595.1; PID:9268
 A:Experimental source: strain B31
 C:Superfamily: unassigned tetratricopeptide repeat proteins; tetratricopeptide repeat
 F:742-704/Domain: tetratricopeptide repeat homology #status atypical <TT1>
 F:742-808/Domain: tetratricopeptide repeat homology <TT2>
 F:808-892/Domain: tetratricopeptide repeat homology <TT3>
 F:892-947/Domain: tetratricopeptide repeat homology <TT4>
 F:947-971/Domain: tetratricopeptide repeat homology <TT5>
 F:971-1010/Domain: tetratricopeptide repeat homology <TT6>
 F:1011-1044/Domain: tetratricopeptide repeat homology #status atypical <TT7>

Query Match 7.4% Score 89; DB 2; Length 1119;
 Best Local Similarity 22.8%; Pred. No. 43;
 Matches 58; Conservative 45; Mismatches 101; Indels 50; Gaps 15;

OY 22 MEKNRSLSLKLTDRPREKSKCKP---LMGRV--YLDLPVITSEKLQDKIDLG---- 72
 Db 249 NNNNTTSLKRISSNQKSELSPPSOTTIGRTYR-----STLIKELVETLDDINTGRV 304
 OY 73 -----GVEEFLSKDIS-----YLISNKKFAOTL-----GRIS--VPSPESAY-- 112
 Db 305 TLCKNRKILKIKKSNKFKQVYNELSKSKNKAASMLTLTKIDENLNIPIKQYRK 364
 OY 113 -----TAETTSPPSHD--GSSFKSPDYCLSGKLYLVEKAKR--HDFI--PSNSILSNA 162
 Db 365 EITQDLKDKKQYLEDLAKSVHSIKRIDLENKSR--QAKILNLEFLKNNPNDKASKT 423
 OY 163 LSMGVYKILMIDIRYITQ--KKRELVLKSSSTVSDG--KRGSAQCTTGRILKRP 218
 Db 424 LAQANKIOHLEDLAKSVHSIKRIDLENKSRQATIDNLEFLKNNPNDKASKT 483
 OY 219 FVKEVEMSGSPAVH 232
 Db 484 IOHLEDLAKSK--VH 495

RESULT 11
 B70242
 conserved hypothetical protein BB19 - Lyme disease spirochete plasmid I/1p28-4
 C:Species: Borrelia burgdorferi (Lyme disease spirochete)
 C>Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 08-Oct-1999
 C:Accession: B70242
 R:Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; Wh
 son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vu
 ; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
 Nature 390, 580-586, 1997
 A:Authors: Smith, H.O.; Venter, J.C.
 A>Title: Genomic sequence of a Lyme disease spirochete, Borrelia burgdorferi.
 A:Reference number: A70100; MUID:98065943
 A:Accession: B70242
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-392 <KLE>
 A:Cross-references: GB:AE000789; NID:92690079; PID:AMC66184.1; PID:92690081; TIGR:BB
 A:Experimental source: strain B31
 C:Genetics:
 A:Genome: plasmid
 C:Superfamily: Lyme disease spirochete plasmid conserved hypothetical protein BB06

Query Match 7.3% Score 87.5; DB 2; Length 392;


```
QY 55 -LPSVTISEKLOKIDKLGVEEPLSKD-----ISYLISNKEAKFAOTLGRISVP 106
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 94 GVEEYISPLSAKEVKD-----QLMSKDKTVLMPVTITGSDKAEKIADETIYL--VP 145
QY 107 SPESAVTAETT-----SPHSHDGSSFKSPDVCISRGKILVEKAIKDHFIP----- 154
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 146 DDLIAITGASLINDPFAHSECEKTEKTEITVCLIGLLIVFRSVTPPEITPIVVGFS 205
QY 155 ---SNSILSNALMGVKILHD 173
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 206 YLISOSIL-----GILVYNVD 221
```

RESULT 15

```
F82315
Conserved hypothetical protein VC0503 [Imported] - Vibrio cholerae (strain N16961 serogr
C:Species: Vibrio cholerae
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C:Accession: F82315
C:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
Hardison, D.; Karpman, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers, F.
I.; R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: AB2035; MUID:20406833
A:Accession: F82315
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-426 <HEI>
A:Cross-references: GR:AE004136; GB:AE003852; NID:99654921; PIDN:AAF93673.1; GSPDB:GN001
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VC0503
A:Map position: 1
```

```
Query Match 7.2%; Score 87; DB 2; Length 426;
Best Local Similarity 24.1%; Pred. No. 18;
Matches 46; Conservative 28; Mismatches 67; Indels 50; Gaps 9;
```

```
QY 60 ISEKLOKIDKLGVEEPLSKDISYL--ISNKEAKFAOTLGRISVPSPESAVTAETT 117
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 229 ISFKLAK-----GVSAFLAEDGFRFYDRAGNSLERAFNR-----YPV---DKAYROIIS 274
QY 118 SPHS-----HDGSSFKSP---DTVCLSRGKILVEKAIKDHFIPSPISNAL 163
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 275 GFNPKRKHPTGVRVPTGDFATPIGAPVYSTGDGKVIY---VRHHPYAGNYLVIEHNS 331
QY 164 SMGVKILIHIDIRYIEQKKKELYLKKSSTSVHDGKRVGSGAOKTFGRGLKRPYKVE 223
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 332 VYKTRRYLHDKI-----LVKKGOLVRGOKIALAGA---TGRLTGPHLHFE 374
QY 224 DMSQSPAVHLH 234
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 375 VLVRNRPPVDM 385
```

Search completed: December 27, 2001, 16:54:46
Job time: 276 sec